



TECH CENTER 1600 42900

RECEIVED

APR 13 2001

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Clinton, Gail M., Adam Evans and William Henner

(ii) TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: DAVIS WRIGHT TREMAINE
- (B) STREET: 1501 Fourth Avenue, 2600 Century Square
- (C) CITY: Seattle
- (D) STATE: Washington
- (E) COUNTRY: U.S.A.
- (F) ZIP: 98101

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: PC compatible
- (C) OPERATING SYSTEM: Windows95
- (D) SOFTWARE: Word

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/506,079
- (B) FILING DATE: 16 February 2000
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Davison, Barry L.
- (B) REGISTRATION NUMBER: 47,309
- (C) REFERENCE/DOCKET NUMBER: 49321-16

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 206 628 7621
- (B) TELEFAX: 206 628 7699

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: HER-2 ECD antagonist

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gly	Xaa	His	Ser	Xaa	Xaa	Pro	Arg	Pro	Ala	Ala	Val	Pro	Val	Pro	Xaa
						5			10					15	
Arg	Xaa	Gln	Pro	Xaa	Pro	Ala	His	Pro	Val	Leu	Ser	Phe	Leu	Arg	Pro
						20			25					30	
Ser	Trp	Asp	Xaa	Val	Ser	Ala	Phe	Tyr	Ser	Leu	Pro	Leu	Ala	Pro	Leu
						35			40				45		
Ser	Pro	Thr	Ser	Val	Xaa	Ile	Ser	Pro	Val	Ser	Val	Gly	Arg	Gly	Xaa
						50			55			60			
Asp	Pro	Asp	Ala	His	Val	Ala	Val	Xaa	Leu	Ser	Arg	Tyr	Glu	Gly	
						65			70			75			

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Leu	Ala	Ala	Leu	Cys	Arg	Trp	Gly	Leu	Leu	Leu	Ala	Leu	Leu
									5		10			15	
Pro	Pro	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Cys	Lys
									20		25			30	
Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met	Leu	Arg	His
									35		40			45	
Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu	Leu	Thr	Tyr
									50		55			60	
Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val
									65		70			75	
Gln	Gly	Tyr	Val	Leu	Cys	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu
									85		90			95	
Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr
									100		105			110	
Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Agn	Agn	Thr	Thr	Pro
									115		120			125	
Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser
									130		135			140	
Leu	Thr	Glu	Cys	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln
									145		150			155	
Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn
									165		170			175	
Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys
									180		185			190	
His	Pro	Cys	Ser	Pro	Cys	Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser

195	200	205
Ser	Glu	Asp
Cys	Gln	Ser
Leu	Thr	Arg
210	215	220
Ala	Arg	Cys
Lys	Gly	Pro
Gly	Pro	Leu
225	230	235
Ala	Ala	Gly
Cys	Thr	Gly
His	Phe	Asn
His	His	Ser
Gly	Ile	Cys
260	265	270
Thr	Tyr	Asn
Thr	Asp	Thr
Phe	Glu	Ser
275	280	285
Tyr	Thr	Phe
Gly	Ala	Ser
Cys	Val	Thr
290	295	300
Ser	Thr	Asp
Val	Gly	Ser
305	310	315
Glu	Val	Thr
Ala	Glu	Asp
Gly	Thr	Gln
325	330	335
Pro	Cys	Ala
Arg	Gly	Xaa
His	Ser	Xaa
340	345	350
Pro	Val	Pro
Xaa	Arg	Xaa
Gln	Pro	Xaa
355	360	365
Phe	Leu	Arg
Pro	Ser	Trp
Asp	Xaa	Val
370	375	380
Leu	Ala	Pro
Leu	Asp	Pro
385	390	395
Gly	Arg	Gly
Xaa	Xaa	Asp
405	410	415
Tyr	Glu	Gly

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGAGCACCAT GGAGCTGGC 19

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCCGGCAGAA ATGCCAGGCT CC 22

- (2) INFORMATION FOR SEQ ID NO:5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AACACAGCGG TGTGAGAAGT GC 22

- (2) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATACCGGGAC AGGTCAACAG C 21

- (2) INFORMATION FOR SEQ ID NO:7:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCTGGGTACC CACTCACTGC 20

- (2) INFORMATION FOR SEQ ID NO:8:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCACACTGG CACGTCCAGA CC 22

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCACGGATCC ATAGCAGACT GAGGAGG 27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGT WCC CAC TCA CYG CYC CCG AGG CCA GCT GCA GTT CCT GTC CCT 45
Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val Pro Val Pro
5 10 15

CWG CGC ATR CAG CCT GNC CCA GCC CAC CCT GTC CTA TCC TTC CTC 90
Xaa Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser Phe Leu
20 25 30

AGA CCC TCT TGG GAC MTA GTC TCT GCC TTC TAC TCT CTA CCC CTG 135
Arg Pro Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro Leu
35 40 45

GCC CCC CTC AGC CCT ACA AGT GTC CST ATA TCC CCT GTC AGT GTG 180
Ala Pro Leu Ser Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val
50 55 60

GGG AGG GGC CYG GAC CCT GAT GCT CAT GTG GCT GTT SAC CTG TCC 225
Gly Arg Gly Xaa Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser
65 70 75

CGG TAT GAA GGC TGA 240
Arg Tyr Glu Gly